IN THE CLAIMS:

Claims 8-12 were previously cancelled. Claims 1, 6, 7, 15, and 16 are cancelled herein. Claims 2-5, 13, and 14 have been amended herein. New claims 17-36 have been added. All of the pending claims are presented below. This listing of claims will replace all prior versions and listings of claims in the application. Please enter these claims as amended.

Listing of the Claims:

1. (Cancelled).

2. (Currently amended) The method according to claim ~~1~~ 17, wherein said complex mixture ~~of~~ comprising proteins and/or peptides is a complex mixture of proteins.

3. (Currently amended) The method according to claim 2, further comprising the cleavage of said complex mixture ~~of~~ comprising proteins into a protein peptide mixture before performing ~~step (b)~~ the first chromatographic step.

4. (Currently amended) The method according to claim ~~1~~ 17, wherein said complex mixture ~~of~~ comprising proteins and/or peptides is a protein peptide mixture.

5. (Currently amended) The method according to claim ~~1~~ 17, further comprising ~~the step of~~ identifying the at least one interaction partner.

6.-12. (Cancelled).

13. (Currently amended) The method according to claim ~~1~~ 17, wherein the ~~compound~~ molecule is a drug, a drug in development, a drug lead, a drug analogue, or a drug derivative.

14. (Currently amended) The method according to claim ~~1~~ 17, wherein ~~the~~ multiple non-neighboring fractions ~~of the primary~~ obtained from the first chromatographic ~~separation obtained in~~ step ~~(b)~~ are pooled prior to the second chromatographic step ~~to combine a plurality of said fractions having distinct elution times into a plurality of pooled fractions, prior to the second chromatographic step~~.

15.-16. (Canceled).

17. (New) A method of isolating in a fraction at least one interaction partner of a molecule out of a complex mixture comprising proteins and/or peptides, wherein the at least one interaction partner is a protein and/or peptide in the complex mixture, and wherein the molecule forms a molecule-interaction partner complex with at least one of the proteins and/or peptides in the complex mixture, the method comprising:

admixing a plurality of the molecules with the complex mixture, wherein each molecule is capable of specifically and stably interacting with a protein or peptide therein to form molecule-interaction partner complexes, wherein molecules thereof do interact with a protein or peptide to form molecule-interaction partner complexes therein, and wherein the specificity of the interaction between the molecule and the protein or peptide in each molecule-interaction partner complex is determined by binding to an active site of the protein or peptide;

separating the resulting admixture into multiple fractions in a first chromatographic step, wherein proteins and/or peptides and molecule-interaction partner complexes are present in a first fraction obtained from the first chromatographic step;

chemically and/or enzymatically altering in the first fraction or another fraction obtained from the first chromatographic step, the molecule present in at least one molecule-interaction partner complex to form at least one altered molecule-interaction partner complex; and

separating at least one fraction comprising at least one altered molecule-interaction partner complex in a second chromatographic step, wherein the first and second chromatographic steps are performed with the same or a substantially similar type of chromatography, and

wherein the at least one altered molecule-interaction partner complex elutes at a different elution time than does the same non-altered molecule-interaction partner complex in the second chromatographic separation, thereby isolating, in a fraction, at least one interaction partner of the molecule.

18. (New) The method according to claim 17, wherein the molecule comprises a chemically reactive group by which the molecule and the protein or peptide in each molecule-interaction partner complex may be cross-linked, wherein the molecule comprises a chemical structure by which the molecule binds to an active site of the protein or peptide in each molecule-interaction partner complex, and wherein the chemically reactive group and the chemical structure are different.

19. (New) The method according to claim 17, wherein the active site of the protein or peptide that determines the specificity of the interaction between the molecule and the protein or peptide is unknown.

20. (New) The method according to claim 17, wherein the at least one protein and/or peptide can only form molecule-interaction partner complexes with the molecule when the at least one protein and/or peptide are in a particular conformation.

21. (New) The method according to claim 13, wherein the drug, drug in development, drug lead, drug analogue, or drug derivative specifically and stably interacts with at least one of the proteins and/or peptides at a concentration of the drug, drug in development, drug lead, drug analogue, or drug derivative that provides a therapeutic effect to a subject.

22. (New) The method according to claim 5, wherein identifying at least one interaction partner is performed using a method selected from the group consisting of mass spectrometry, electrophoresis, activity measurement, immunochemistry, and Edman sequencing.

23. (New) The method according to claim 22, wherein identifying at least one interaction partner is performed using mass spectrometry selected from the group consisting of tandem mass spectrometry and Post-Source Decay analysis.

24. (New) The method according to claim 5, wherein identifying at least one interaction partner is performed by a method comprising measuring the mass of the at least one interaction partner.

25. (New) The method according to claim 17, wherein the complex mixture comprising proteins and/or peptides is selected from the group consisting of cell lysates, microsomal fractions, cell fractions, tissues, organelles, urine, sputum, saliva, synovial fluid, nipple aspiration fluid, amnion fluid, blood, cerebrospinal fluid, tears, ejaculate, serum, pleural fluid, ascites fluid, stool, and biopsy samples.

26. (New) The method according to claim 17, further comprising treating the complex mixture comprising proteins and/or peptides to remove contaminants prior to admixing the plurality of the molecules with the complex mixture.

27. (New) The method according to claim 5, further comprising identifying the interaction site within the at least one interaction partner.

28. (New) The method according to claim 17, wherein the interaction partner is selected from the group consisting of a polypeptide, a nucleoprotein, a glycopeptide, an enzyme, a hormone, a transcription factor, a receptor, a peptide ligand for a receptor, a growth factor, an immunoglobulin, a steroid receptor, a nuclear protein, a hydrolase, a dehydrogenase, a ligase, and a transferase.

29. (New) The method according to claim 17, wherein the molecule-interaction partner complex is a penicilloyl-peptide.

30. (New) The method according to claim 17, wherein the molecule is cross-linked to the interaction partner in the molecule-interaction partner complex by catalytic action of a transglutaminase.

31. (New) The method according to claim 17, wherein the molecule comprises a peptide sequence cleaved by an enzyme, and wherein the at least one altered molecule-interaction partner complex is formed by enzymatic cleavage of the molecule by the enzyme.

32. (New) The method according to claim 31, wherein the enzyme is factor Xa.

33. (New) The method according to claim 17, wherein the molecule comprises an enzyme inhibitory peptide.

34. (New) The method according to claim 33, wherein the enzyme inhibitory peptide is a caspase inhibitory peptide.

35. (New) The method according to claim 17, wherein the active site is an adenosine triphosphate binding site.

36. (New) The method according to claim 35, wherein the interaction partner is a kinase that is capable of hydrolyzing adenosine triphosphate.